



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/507,106

DATE: 09/21/2004
TIME: 09:27:01

Input Set : A:\26352U sequence listing.ST25.txt
Output Set: N:\CRF4\09212004\J507106.raw

3 <110> APPLICANT: Japan Science and Technology Agency
5 <120> TITLE OF INVENTION: Gene participating in the synthesis of brassinosteroid
7 <130> FILE REFERENCE: 26352U (PS03-311PCT)
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/507,106
C--> 9 <141> CURRENT FILING DATE: 2004-09-10
9 <160> NUMBER OF SEQ ID NOS: 6
11 <170> SOFTWARE: PatentIn version 3.1
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 1473
15 <212> TYPE: DNA
16 <213> ORGANISM: Arabidopsis thaliana
18 <400> SEQUENCE: 1

19 atggacactt cttcttact ttgttcttc tccttcttct tctttatcat catcgcatc	60
21 ttcaacaaga tcaacggctc cagatcatcc ccagcttcaa agaaaaaaact taatgatcat	120
23 catgttacat cccagagtca cggaccaaag ttccacacg gaagcttggg atggccgtc	180
25 atcggtgaaa ccatcgagtt cgtcttctc gcttactcag accgtcctga gagttcatg	240
27 gacaagcgtc gtctcatgtt tggagagtg tttaagtcgc atattttgg aacggcgacg	300
29 atcgtgtcga cggatgctga agtgaacaga gccgtttac agagcgactc gacagcttc	360
31 gtgccgtttt acccaaaaac ggtaaaggag ctaatggaa aatcgctcat acttcttac	420
33 aacgggagtt tacatagacg gttccatggg ttagtcgtt ctttcttaaa gtcgccactt	480
35 ctc当地 aatcgtagt agacatgcac aagttttgt cggaaatccat ggatctatgg	540
37 tccgaggacc aacctgtgct cctccaagac gtctccaaga ctgttgcatt caaagtactt	600
39 gccaaggcat tgataagtgt agagaaaggaa gaagatttag aagagctaaa gagagagttt	660
41 gaaaatttca tatcaggact catgtcatta ccaattaact tccctggAAC gcaactccat	720
43 agatctctcc aagctaagaa gaatatggtg aagcaagttg aaagaatcat agaaggcaaa	780
45 attaggaaaa caaagaacaa ggaggaagat gatgttattt caaaggatgt tgtgatgtg	840
47 ttgcttaagg actcaagtga acatTTTact cacaatttga ttgcttaacaa tatgatcgac	900
49 atgatgatcc ctggccacga ttctgtccct gtcctcatta ccctggcgt caaattcctc	960
51 tctgattctc ctgctgcctt caatctccta acgaaaaaca tgaagctgaa aagtttgaag	1020
53 gaattgacag gagagccact atattggaaat gactacttgt cgttacctt aacacaaaag	1080
55 gtgattacag agacactgag aatgggaaat gttataattt gagtgtatgag aaaggcgatg	1140
57 aaagatgttggaaataatgtata ccaaaggat ggtgtttttt ggcctatctc	1200
59 agatcgttc atcttgcattt gacttattt gacttccgt acaaattttaa tccctggaga	1260
61 tggcaagaaa gggacatgaa cacgagtagt ttctgtccctt ttggaggtgg tcagagattt	1320
63 tgccctggtc tcgatttggc tcgtcttggaa acttcagttt ttcttccacca ttgttact	1380
65 cgcttcagat ggatagcaga agaagacaca atcataaaact tcccaacgggt gcatatgaag	1440
67 aacaaatttac ccatttggat caaaaagaataa taa	1473

70 <210> SEQ ID NO: 2
71 <211> LENGTH: 490
72 <212> TYPE: PRT
73 <213> ORGANISM: Arabidopsis thaliana
75 <400> SEQUENCE: 2
77 Met Asp Thr Ser Ser Ser Leu Leu Phe Phe Ser Phe Phe Phe Ile



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78 1	5	10	15
81 Ile Ile Val Ile Phe Asn Lys Ile Asn Gly Leu Arg Ser Ser Pro Ala			
82	20	25	30
85 Ser Lys Lys Lys Leu Asn Asp His His Val Thr Ser Gln Ser His Gly			
86	35	40	45
89 Pro Lys Phe Pro His Gly Ser Leu Gly Trp Pro Val Ile Gly Glu Thr			
90	50	55	60
93 Ile Glu Phe Val Ser Ser Ala Tyr Ser Asp Arg Pro Glu Ser Phe Met			
94 65	70	75	80
97 Asp Lys Arg Arg Leu Met Tyr Gly Arg Val Phe Lys Ser His Ile Phe			
98	85	90	95
101 Gly Thr Ala Thr Ile Val Ser Thr Asp Ala Glu Val Asn Arg Ala Val			
102	100	105	110
105 Leu Gln Ser Asp Ser Thr Ala Phe Val Pro Phe Tyr Pro Lys Thr Val			
106	115	120	125
109 Arg Glu Leu Met Gly Lys Ser Ser Ile Leu Leu Ile Asn Gly Ser Leu			
110	130	135	140
113 His Arg Arg Phe His Gly Leu Val Gly Ser Phe Leu Lys Ser Pro Leu			
114 145	150	155	160
117 Leu Lys Ala Gln Ile Val Arg Asp Met His Lys Phe Leu Ser Glu Ser			
118	165	170	175
121 Met Asp Leu Trp Ser Glu Asp Gln Pro Val Leu Leu Gln Asp Val Ser			
122	180	185	190
125 Lys Thr Val Ala Phe Lys Val Leu Ala Lys Ala Leu Ile Ser Val Glu			
126	195	200	205
129 Lys Gly Glu Asp Leu Glu Glu Leu Lys Arg Glu Phe Glu Asn Phe Ile			
130	210	215	220
133 Ser Gly Leu Met Ser Leu Pro Ile Asn Phe Pro Gly Thr Gln Leu His			
134 225	230	235	240
137 Arg Ser Leu Gln Ala Lys Lys Asn Met Val Lys Gln Val Glu Arg Ile			
138	245	250	255
141 Ile Glu Gly Lys Ile Arg Lys Thr Lys Asn Lys Glu Glu Asp Asp Val			
142	260	265	270
145 Ile Ala Lys Asp Val Val Asp Val Leu Leu Lys Asp Ser Ser Glu His			
146	275	280	285
149 Leu Thr His Asn Leu Ile Ala Asn Asn Met Ile Asp Met Met Ile Pro			
150	290	295	300
153 Gly His Asp Ser Val Pro Val Leu Ile Thr Leu Ala Val Lys Phe Leu			
154 305	310	315	320
157 Ser Asp Ser Pro Ala Ala Leu Asn Leu Leu Thr Lys Asn Met Lys Leu			
158	325	330	335
161 Lys Ser Leu Lys Glu Leu Thr Gly Glu Pro Leu Tyr Trp Asn Asp Tyr			
162	340	345	350
165 Leu Ser Leu Pro Leu Thr Gln Lys Val Ile Thr Glu Thr Leu Arg Met			
166	355	360	365
169 Gly Asn Val Ile Ile Gly Val Met Arg Lys Ala Met Lys Asp Val Glu			
170	370	375	380
173 Ile Lys Gly Tyr Val Ile Pro Lys Gly Trp Cys Phe Leu Ala Tyr Leu			
174 385	390	395	400

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177 Arg Ser Val His Leu Asp Glu Ala Tyr Tyr Glu Ser Pro Tyr Lys Phe
178 405 410 415
181 Asn Pro Trp Arg Trp Gln Glu Arg Asp Met Asn Thr Ser Ser Phe Ser
182 420 425 430
185 Pro Phe Gly Gly Gln Arg Leu Cys Pro Gly Leu Asp Leu Ala Arg
186 435 440 445
189 Leu Glu Thr Ser Val Phe Leu His His Leu Val Thr Arg Phe Arg Trp
190 450 455 460
193 Ile Ala Glu Glu Asp Thr Ile Ile Asn Phe Pro Thr Val His Met Lys
194 465 470 475 480
197 Asn Lys Leu Pro Ile Trp Ile Lys Arg Ile
198 485 490
201 <210> SEQ ID NO: 3
202 <211> LENGTH: 1934
203 <212> TYPE: DNA
204 <213> ORGANISM: Arabidopsis thaliana
206 <220> FEATURE:
207 <221> NAME/KEY: misc_feature
208 <222> LOCATION: (1748)..(1748)
209 <223> OTHER INFORMATION: n means A, C, G or T.
212 <400> SEQUENCE: 3
213 ttgtcttagg catataggta ttcccaagaa accggtttaa ctgtttacgt atgcaacctc 60
215 cggcaagcgc aggactttc cggtcgccgg aaaatctccc ttggccttat aattacatgg 120
217 attatttggc cgctggttc ttgggtttga cggccggaat acttctccgt ccatggctct 180
219 ggtttcgtct acgaaactcg aaaacgaaag atggagatga agaagaagat aatgaggaga 240
221 agaagaaggg aatgattcca aacggaagct taggctggcc ggtgatcgga gaaaccctaa 300
223 acttcatcgc ttgtggttat tcttctcgcc ctgttacctt catggacaaa cgaaagtctt 360
225 tatacggaa agtgttcaaa acgaacataa tagggacacc aatcataata tcaaccgatg 420
227 cagaggtgaa taaagtggtg ctccaaaacc atggAACAC atttgcctt gcatacccta 480
229 aatcaattac ggaactactt ggagaaaact ctattctcg catcaatgg cctcatcaa 540
231 aaaggcttca cacgctcatt ggcgcgttcc tcagatctcc tcacctcaaa gaccggatca 600
233 ctcgagacat tgaggcctcg gttgttctca ctttggcgtc ttggcctcaa cttccattgg 660
235 ttcatgttca ggatgagatc aaaaagatga cgttttagat attagtaaaa gtgtttagat 720
237 gcacatctcc tggtaagat atgaacattc tcaaacttga gttcgaagaa ttcatcaaag 780
239 gtttgatttg tatcccaatc aaattccctg gcactagact ctacaaatcc ttaaaggcga 840
241 aagagaggt aataaagatg gtaaaaaagg ttgtggagga gagacaagtg gcgatgacaa 900
243 cgacgtctcc ggcaaatgac gtggggacg tacttctaa agacgggtgt gatcagaga 960
245 agcaatctca accgtcagat ttgcgtcagcg gaaagatcg agagatgtg atacccggag 1020
247 agggaaacaat gccaacggcg atgaccttgg ctgtcaaatt cttaagtgcg aaccccgatcg 1080
249 ctctagccaa actcggtggag gagaatatgg agatgaagag gcgttaatttgcgaaatgg 1140
251 aagaatacaa gtggaccgat tataatgttcc tctcttttac tcaaaatgtg ataaacgaaa 1200
253 cgcttagaat ggcttaacatt attaacgggg tggggaggaa agctctcaag gatgttagaaa 1260
255 ttaaagggtt cttataccg aaaggatggt gtgtattggc atcattcata tcgggttcaca 1320
257 tggatgaaga catttatgtat aatccctatc aattcgatcc gtggagatgg gacagaattt 1380
259 atggatcgcc aaacagcagt atttgcttca caccctttgg tgggtggccaa aggctatgtc 1440
261 ctggttttaga gctgtcgaag ctcgaaatat ccattttct tcaccacctt gtaaccccgatcg 1500
263 acagttggac ggctgaggaa gacgagatag tggcatttcc gactgtgaag atgaagcggaa 1560
265 ggctcccgat ccgagttggct actgttagatg atagtgcctt tccgatctca cttgaagatc 1620
267 attaatagat catttcaaag aacaaaactg tttgtcaaa gaggaagcag agaagtaaac 1680

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269 aaatgatctt attaacaat agtagagaag agaagcaaac aagattggtg ggtaagacag 1740
W--> 271 aaagaacnaa acgtacagct agtcatggct caaagatgag agattctaat tataatttt 1800
273 tttgttgc atgtcaaatt ataagcgttg gtttaggtgt ccctttctct tttatatttc 1860
275 gtaccaaacg caagttgaga tatgattcca tatatatgga tgatagatat gtatattaaat 1920
277 atatacgccg cggg 1934
280 <210> SEQ ID NO: 4
281 <211> LENGTH: 524
282 <212> TYPE: PRT
283 <213> ORGANISM: Arabidopsis thaliana
285 <400> SEQUENCE: 4
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288 1 5 10 15
291 Pro Trp Pro Tyr Asn Tyr Met Asp Tyr Leu Val Ala Gly Phe Leu Val
292 20 25 30
295 Leu Thr Ala Gly Ile Leu Leu Arg Pro Trp Leu Trp Phe Arg Leu Arg
296 35 40 45
299 Asn Ser Lys Thr Lys Asp Gly Asp Glu Glu Asp Asn Glu Glu Lys
300 50 55 60
303 Lys Lys Gly Met Ile Pro Asn Gly Ser Leu Gly Trp Pro Val Ile Gly
304 65 70 75 80
307 Glu Thr Leu Asn Phe Ile Ala Cys Gly Tyr Ser Ser Arg Pro Val Thr
308 85 90 95
311 Phe Met Asp Lys Arg Lys Ser Leu Tyr Gly Lys Val Phe Lys Thr Asn
312 100 105 110
315 Ile Ile Gly Thr Pro Ile Ile Ile Ser Thr Asp Ala Glu Val Asn Lys
316 115 120 125
319 Val Val Leu Gln Asn His Gly Asn Thr Phe Val Pro Ala Tyr Pro Lys
320 130 135 140
323 Ser Ile Thr Glu Leu Leu Gly Glu Asn Ser Ile Leu Ser Ile Asn Gly
324 145 150 155 160
327 Pro His Gln Lys Arg Leu His Thr Leu Ile Gly Ala Phe Leu Arg Ser
328 165 170 175
331 Pro His Leu Lys Asp Arg Ile Thr Arg Asp Ile Glu Ala Ser Val Val
332 180 185 190
335 Leu Thr Leu Ala Ser Trp Ala Gln Leu Pro Leu Val His Val Gln Asp
336 195 200 205
339 Glu Ile Lys Lys Met Thr Phe Glu Ile Leu Val Lys Val Leu Met Ser
340 210 215 220
343 Thr Ser Pro Gly Glu Asp Met Asn Ile Leu Lys Leu Glu Phe Glu Glu
344 225 230 235 240
347 Phe Ile Lys Gly Leu Ile Cys Ile Pro Ile Lys Phe Pro Gly Thr Arg
348 245 250 255
351 Leu Tyr Lys Ser Leu Lys Ala Lys Glu Arg Leu Ile Lys Met Val Lys
352 260 265 270
355 Lys Val Val Glu Glu Arg Gln Val Ala Met Thr Thr Ser Pro Ala
356 275 280 285
359 Asn Asp Val Val Asp Val Leu Leu Arg Asp Gly Gly Asp Ser Glu Lys
360 290 295 300
363 Gln Ser Gln Pro Ser Asp Phe Val Ser Gly Lys Ile Val Glu Met Met

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364	305	310	315	320
367	Ile Pro Gly Glu Glu Thr Met Pro Thr Ala Met Thr Leu Ala Val Lys			
368	325	330	335	
371	Phe Leu Ser Asp Asn Pro Val Ala Leu Ala Lys Leu Val Glu Glu Asn			
372	340	345	350	
375	Met Glu Met Lys Arg Arg Lys Leu Glu Leu Gly Glu Glu Tyr Lys Trp			
376	355	360	365	
379	Thr Asp Tyr Met Ser Leu Ser Phe Thr Gln Asn Val Ile Asn Glu Thr			
380	370	375	380	
383	Leu Arg Met Ala Asn Ile Asn Gly Val Trp Arg Lys Ala Leu Lys			
384	385	390	395	400
387	Asp Val Glu Ile Lys Gly Tyr Leu Ile Pro Lys Gly Trp Cys Val Leu			
388	405	410	415	
391	Ala Ser Phe Ile Ser Val His Met Asp Glu Asp Ile Tyr Asp Asn Pro			
392	420	425	430	
395	Tyr Gln Phe Asp Pro Trp Arg Trp Asp Arg Ile Asn Gly Ser Ala Asn			
396	435	440	445	
399	Ser Ser Ile Cys Phe Thr Pro Phe Gly Gly Gln Arg Leu Cys Pro			
400	450	455	460	
403	Gly Leu Glu Leu Ser Lys Leu Glu Ile Ser Ile Phe Leu His His Leu			
404	465	470	475	480
407	Val Thr Arg Tyr Ser Trp Thr Ala Glu Glu Asp Glu Ile Val Ser Phe			
408	485	490	495	
411	Pro Thr Val Lys Met Lys Arg Arg Leu Pro Ile Arg Val Ala Thr Val			
412	500	505	510	
415	Asp Asp Ser Ala Ser Pro Ile Ser Leu Glu Asp His			
416	515	520		
419	<210> SEQ ID NO: 5			
420	<211> LENGTH: 20			
421	<212> TYPE: DNA			
422	<213> ORGANISM: Artificial sequence			
424	<220> FEATURE:			
425	<223> OTHER INFORMATION: PCR amplification primer			
427	<400> SEQUENCE: 5			
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431	<210> SEQ ID NO: 6			
432	<211> LENGTH: 21			
433	<212> TYPE: DNA			
434	<213> ORGANISM: Artificial sequence			
436	<220> FEATURE:			
437	<223> OTHER INFORMATION: PCR amplification primer			
439	<400> SEQUENCE: 6			
440	tgattttatat tcttttgatc c		21	

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 09/21/2004
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Input Set : A:\26352U sequence listing.ST25.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 1748

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:1740